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Lead System Transformation for Pooling of Body Surface Map Data: a Surface Laplacian Approach

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Abstract

In this paper, a method is described to transform Body Surface Map (BSM) data from one lead system to that of another. This enables pooling of BSM data between different centres. The transformation tool is based upon Laplacian interpolation. It is evaluated by inspecting transformations from lead systems having few leads to one having many leads.

Keywords: body surface mapping, Laplacian interpolation, lead system transformation

Introduction

One of the goals of the European Committee's concerted action NEMY (Noninvasive Evaluation of the MYocardium) [1] is the pooling of Body Surface Map (BSM) data between the research groups involved in NEMY: the universities of Parma, Brussels, Bath, Nijmegen and Helsinki. A major problem concerning this pooling is that each group uses a completely different lead system, different both in the lead positioning and in the number of leads (Parma: 219, Brussels: 120, Helsinki: 123, Nijmegen: 64 and Bath: 40).

In this paper, a transformation tool is described by which BSM data from one group can be converted to the lead system of another group. Furthermore, a first evaluation of the tool is carried out.

The basis of the transformation technique proposed is the interpolation of potentials on a triangulated closed surface as described in [2].

Methods

A series of BSM data can be represented as a matrix M in which each column represents the spatial potential distribution at a single time instant and each row represents an ECG at a single lead. This matrix thus contains a complete 'movie' of measurements at all leads at different time instants. Transformation of the BSM in a certain lead system format to that of another can be carried out by multiplying this BSM with a suitable transformation matrix. A new data matrix is obtained for the desired lead system as:

$$M_B = T_{BA} M_A, \quad (1)$$

in which M_A is the original map (dimension $n \times t$, with n being the number of leads used in system A and t the number of time samples), T_{BA} the transfer matrix (dimension $m \times n$, with m the number of leads in system

B), and M_B the resulting map (dimension $m \times t$) in the format of system B.

The transformation matrix T_{BA} is obtained in two steps: first, the transformation matrix T_F from the original BSM to the potential distribution on a densely triangulated torso surface is computed, and second, the transformation matrix T_E from the full torso potential distribution to the new lead potentials is derived. So, $T_{BA} = T_E T_F$. T_F has dimension $\ell \times n$ (ℓ being the total number of vertices on the triangulated torso) and T_E has dimension $m \times \ell$.

Matrix T_E is constructed in such a way that each row represents an operator performing a linear interpolation between the vertices of the triangle on which an electrode site is defined.

Matrix T_F is derived by constructing the surface Laplacian operator L on the triangulation of the full torso [2]. Characteristic for a *smooth* potential distribution is that the expression $L\varphi$, with φ being the potentials on the torso, is small: $L\varphi \approx 0$. φ can be made to satisfy this near-equality by solving the equation $L\varphi = 0$ in a least squares sense. The equation can be rewritten, after subdividing L and φ into parts corresponding to the known lead potentials φ_1 and parts corresponding to the unknown potentials φ_2 :

$$\begin{bmatrix} L_{12} \\ L_{22} \end{bmatrix} \varphi_2 = - \begin{bmatrix} L_{11} \\ L_{21} \end{bmatrix} \varphi_1. \quad (2)$$

φ_2 can be computed by matrix-multiplication once the inverse of $\begin{bmatrix} L_{12} \\ L_{22} \end{bmatrix}$ is known. Because this matrix is not square, only a pseudo-inverse can be obtained, for example by using singular value decomposition. Thus, after computation of φ_2 , the full torso potential distribution φ is known. In short, T_F can be written as:

$$T_F = \begin{bmatrix} I_{11} \\ - \begin{bmatrix} L_{12} \\ L_{22} \end{bmatrix}^\dagger \begin{bmatrix} L_{11} \\ L_{21} \end{bmatrix} \end{bmatrix}, \quad (3)$$

where I_{11} is the ($n \times n$) identity matrix and the \dagger denotes the pseudo-inverse operator.

The matrix T_E was created by using the following algorithm: a triangulation was made based on MR images of the torso of one of the subjects, currently available to our group. For each lead system involved, an algorithm was

constructed to position the electrodes to this triangulated torso in the same way laborants attach them in real life.

Using the lead system definition and the triangulation, T_F was computed and subsequently, T_{BA} for each system.

For a first evaluation of the transformation matrices, BSM data were created, by multiplying simulated full torso BSM data by T_E for each lead system. The full torso BSM data were generated by forward simulation of an inverse solution, obtained as described in [3]. The BSM data created for each system were transformed to the Parma system, which contains the largest number of leads. The resulting data were compared to those of the Parma lead system, using the Relative Difference [2] defined as

$$RelDif = \sqrt{\frac{\sum (M_1 - M_2)^2}{\sum M_1^2}}, \quad (4)$$

where M_1 is the Parma data computed directly and M_2 the data resulting from the transformation.

Results

An anterior view of the triangulation used to create T_E , T_F and the transformation matrices T_{BA} for each lead system is shown in Figure 1.

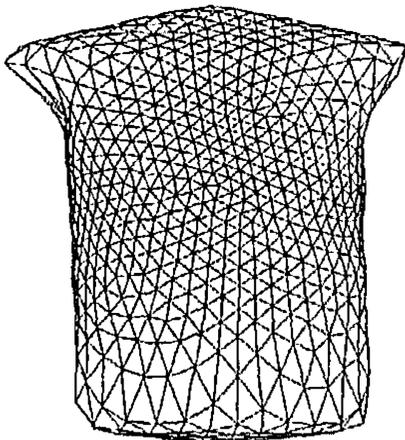


Figure 1. Triangulation used to calculate T_{BA} .

In Figure 2 the lead systems of Parma and Nijmegen are shown on the same torso. The electrodes are depicted as small buttons.

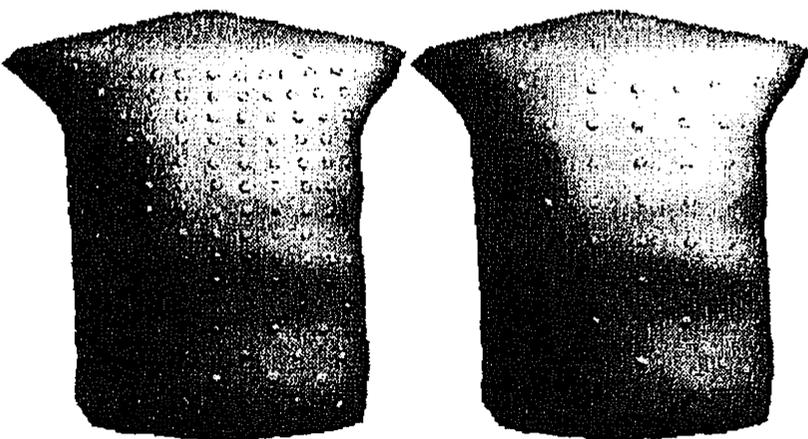


Figure 2. Parma (left) and Nijmegen (right) electrode system, anterior view only.

In Table I, the values of $RelDif$ for transformation of BSM data of several systems to the Parma system is given.

| Parma | Helsinki | Brussels | Nijmegen | Bath |
|-------|----------|----------|----------|--------|
| - | 0.0756 | 0.0753 | 0.1552 | 0.2665 |

Table I. Relative Differences between the Parma BSM and BSMs transformed to the Parma lead system.

In Figure 3, a Parma BSM at mid-QRS and the corresponding result of a transformation from Nijmegen to the Parma lead system are shown.

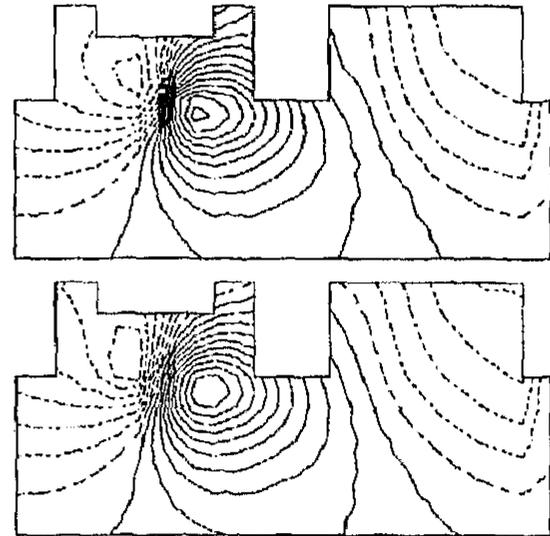


Figure 3. Parma BSM (top) and transformed Nijmegen BSM (bottom), mid-QRS. Isopotential lines are at 0.2 mV intervals, solid: positive, dashed: negative.

Discussion

The transformation tool as described in this paper appears to be a very useful tool to transform Body Surface Map data from one lead system to another. With this tool, the pooling of data originating from different lead systems is possible and multi-center BSM studies can now be carried out.

The lead system yielding the lowest $RelDif$ after transformation to Parma is Brussels, followed by Helsinki, Nijmegen and Bath respectively. This order reflects the decreasing number of leads in the lead systems.

Qualitatively, the Parma map and the transformed Nijmegen map still show a strong resemblance. This is also the case for the transformed maps of other lead systems. It is therefore not clear whether $RelDif$ is the most appropriate measure for the quality of the transformation and if it is, what value of $RelDif$ distinguishes a good transformation from a bad one.

References

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